

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/981,151 D
Source: JFW16
Date Processed by STIC: 08/22/2005

ENTERED



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/981,151D

DATE: 08/22/2005
TIME: 10:02:32

Input Set : D:\Cura 468 SEQ list 0705.txt
Output Set: N:\CRF4\08222005\I981151D.raw

3 <110> APPLICANT: Guo, Xiaoja
 5 <120> TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 7 <130> FILE REFERENCE: 21402-168
 9 <140> CURRENT APPLICATION NUMBER: 09/981,151D
 10 <141> CURRENT FILING DATE: 2001-10-16
 12 <150> PRIOR APPLICATION NUMBER: 60/241,040
 13 <151> PRIOR FILING DATE: 2000-10-17
 15 <150> PRIOR APPLICATION NUMBER: 60/241,058
 16 <151> PRIOR FILING DATE: 2000-10-17
 18 <150> PRIOR APPLICATION NUMBER: 60/241,063
 19 <151> PRIOR FILING DATE: 2000-10-17
 21 <150> PRIOR APPLICATION NUMBER: 60/241,243
 22 <151> PRIOR FILING DATE: 2000-10-17
 24 <150> PRIOR APPLICATION NUMBER: 60/242,152
 25 <151> PRIOR FILING DATE: 2000-10-20
 27 <150> PRIOR APPLICATION NUMBER: 60/242,482
 28 <151> PRIOR FILING DATE: 2000-10-23
 30 <150> PRIOR APPLICATION NUMBER: 60/242,611
 31 <151> PRIOR FILING DATE: 2000-10-23
 33 <150> PRIOR APPLICATION NUMBER: 60/242,612
 34 <151> PRIOR FILING DATE: 2000-10-23
 36 <150> PRIOR APPLICATION NUMBER: 60/242,880
 37 <151> PRIOR FILING DATE: 2000-10-24
 39 <150> PRIOR APPLICATION NUMBER: 60/242,881
 40 <151> PRIOR FILING DATE: 2000-10-24
 42 <150> PRIOR APPLICATION NUMBER: 60/259,028
 43 <151> PRIOR FILING DATE: 2000-12-29
 45 <150> PRIOR APPLICATION NUMBER: 60/269,813
 46 <151> PRIOR FILING DATE: 2001-02-20
 48 <150> PRIOR APPLICATION NUMBER: 60/286,324
 49 <151> PRIOR FILING DATE: 2001-04-25
 51 <150> PRIOR APPLICATION NUMBER: 60/294,108
 52 <151> PRIOR FILING DATE: 2001-05-29
 54 <150> PRIOR APPLICATION NUMBER: 60/303,968
 55 <151> PRIOR FILING DATE: 2001-07-09
 57 <160> NUMBER OF SEQ ID NOS: 166
 59 <170> SOFTWARE: PatentIn Ver. 2.1
 61 <210> SEQ ID NO: 1
 62 <211> LENGTH: 2997
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Homo sapiens
 66 <220> FEATURE:
 67 <221> NAME/KEY: misc_feature

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68 <222> LOCATION: (857)..(858)
 69 <223> OTHER INFORMATION: Wherein n is an a or t or c or g.
 71 <220> FEATURE:
 72 <221> NAME/KEY: misc_feature
 73 <222> LOCATION: (2383)
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 77 <221> NAME/KEY: misc_feature
 78 <222> LOCATION: (2983)
 79 <223> OTHER INFORMATION: wherein n is an a or t or c or g.
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 84 tccggacagc tggagggcgag tcccccgccg ctccctctccc gcggaccccg ccgtctcacc 180
 85 gcgatgtcgc cgctgtttc cgccaggcacc tgcgtgcgc atgggaccgg cagcggcagc 240
 86 gcctgggagc ccgagcgtcc cgcttcctcc tccaccccgcc gagcggccgg gctggatgga 300
 87 aaaggcgccg acatggatga agctggaaac catcgttctc agcaaactaa cacaggaaca 360
 88 gaaaacccaa cactgcatgt tctcactcaa tatgacctgg tctctgccta cgagggttgc 420
 89 cacagggcg attacgtgtc ccatgaaatc atgcaccatc agcggcggag aagagcagtg 480
 90 gccgtgtccg aggtttagtc tcttcacctt cggctgaaag gcccaggca cgacttccac 540
 91 atggatctga ggacttccag cagcctagtg gctctggct ttattgtgca gacgttggga 600
 92 aagacaggca ctaagtctgt gcagacttta ccgcaggagg acttctgttt ctatcaaggc 660
 93 tctttgcgtat cacacagaaa ctgcctatcg catggaggga agttctgtga gggctccact 720
 94 cgcaactctga agctctgcaa cagtcagaaa tgtcccgcc acagtgttga ctccgtgct 780
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 102 ctcaacatgg tatctgtttt attcaaagat ggaacaatag gaggaaacat caacattgca 1260
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 107 attaatgaag atacaggtct tggactggcc ttcaccattt cccatgagtc tggacacaac 1560
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 111 aaggaataca agtatcctga gaaattgcca ggagaattat atgatgcaaa cacacagtgc 1800
 112 aagtggcagt tcggagagaa agccaagctc tgcgtctgg actttaaaaa ggacatctgt 1860
 113 aaagccctgt ggtgccatcg tattggaggaa aatgtgaga ctaaatttat gccagcagca 1920
 114 gaaggcacaa tttgtggca tgacatgtgg tggcgccggag gacagtgtgt gaaatatgg 1980
 115 gatgaaggcc ccaagccac ccatggccac tggtcggact ggtcttcttg gtccccatgc 2040
 116 tccaggaccc gcggagggggg agtatctcat aggagtcgc tctgcacccaa ccccaatcca 2100
 117 tcgcgtggag ggaagttctg tgagggctcc actcgcactc tgaagctctg caacagtcag 2160
 118 aaatgtcccc gggacagtgt tgacttcgt gctgctcagt gtgccgagca caacagcaga 2220
 119 cgattcagag ggcggcacta caagtggaaag cctcaggact tatgcaact ctactgtatc 2280

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Input Set : D:\Cura 468 SEQ list 0705.txt
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120 gcagaaggat ttgatttctt ctttccttg tcaaataaaag tcaaagatgg gactccatgc 2340
 121 tcggaggata gccgtaatgt ttgtatagat gggatatgtg agnttggatg tgacaatgtc 2400
 122 cttggatctg atgctgttga agacgtctgt ggggtgtgt a cggaaataa ctcagcctgc 2460
 123 acgattcaca ggggtctcta caccaagcac caccacacca accattatca catggtcacc 2520
 124 attccttctg gagccccgag tatccgcac tatgaaatga acgtctctac ctcctacatt 2580
 125 tctgtgcgca atgcctcag aaggtactac ctgaatgggc actggaccgt ggactggccc 2640
 126 ggcccggtaca aatttcggg cactacttc gactacagac ggtcctataa tgagcccgag 2700
 127 aacttaatcg ctactggacc aaccaacgag acactgattg tggagctgct gttcaggga 2760
 128 aggaaccgg gtgtgcctg ggaataactcc atgcctcgct tggggaccga gaagcagccc 2820
 129 cctggccagc ccagctacac ttggccatc gtgcgtctg agtgcctcggt gtcctgcgg 2880
 130 ggggttaggt gcctccagt gctgctctg gaggcagcat gtcagccttc agccactgog 2940
 131 tacattgcac tggccttct tgaatcctaa tgagcagccc ggngcttctc cctgcca 2997
 134 <210> SEQ ID NO: 2
 135 <211> LENGTH: 986
 136 <212> TYPE: PRT
 137 <213> ORGANISM: Homo sapiens
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 140 <221> NAME/KEY: VARIANT
 141 <222> LOCATION: (283)
 142 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
 144 <220> FEATURE:
 145 <221> NAME/KEY: VARIANT
 146 <222> LOCATION: (792)
 147 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
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 151 1 5 10 15
 153 Leu Leu Ala Gln Val Ala Glu Gln Val Ser Pro Gly Arg Ser His Gln
 154 20 25 30
 156 Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu
 157 35 40 45
 159 Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser
 160 50 55 60
 162 Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
 163 65 70 75 80
 165 Pro Glu Arg Pro Ala Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp
 166 85 90 95
 168 Gly Lys Gly Arg Asp Met Asp Glu Ala Gly Asn His Arg Ser Gln Gln
 169 100 105 110
 171 Thr Asn Thr Gly Thr Glu Asn Gln Thr Leu His Val Leu Thr Gln Tyr
 172 115 120 125
 174 Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser
 175 130 135 140
 177 His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala Val Ser
 178 145 150 155 160
 180 Glu Val Glu Ser Leu His Leu Arg Leu Lys Gly Pro Arg His Asp Phe
 181 165 170 175
 183 His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile
 184 180 185 190

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186 Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro
 187 195 200 205
 189 Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn
 190 210 215 220
 192 Ser Pro Ser His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr Leu
 193 225 230 235 240
 195 Lys Leu Cys Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe Arg
 196 245 250 255
 198 Ala Ala Gln Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg His
 199 260 265 270
 W--> 201 Tyr Lys Trp Lys Pro Tyr Thr Gln Val Glu Xaa Asp Leu Cys Lys Leu
 202 275 280 285
 204 Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Ser Leu Ser Asn Lys
 205 290 295 300
 207 Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile
 208 305 310 315 320
 210 Asp Gly Ile Cys Glu Leu Ser Val Val Ser Thr Ser Ala His Met Pro
 211 325 330 335
 213 Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys Ser
 214 340 345 350
 216 Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu Glu
 217 355 360 365
 219 Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln Asn
 220 370 375 380
 222 His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn Met
 223 385 390 395 400
 225 Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn Ile
 226 405 410 415
 228 Ala Ile Val Gly Leu Ile Leu Glu Asp Glu Gln Pro Gly Leu Val
 229 420 425 430
 231 Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp Gln
 232 435 440 445
 234 Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile Leu
 235 450 455 460
 237 Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp Thr
 238 465 470 475 480
 240 Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser Cys
 241 485 490 495
 243 Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala His
 244 500 505 510
 246 Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn Met
 247 515 520 525
 249 Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly Arg
 250 530 535 540
 252 Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His Lys
 253 545 550 555 560
 255 Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys Pro
 256 565 570 575
 258 Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr Asp

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259	580	585	590
261	Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly Glu Lys Ala Lys Leu Cys		
262	595	600	605
264	Met Leu Asp Phe Lys Lys Asp Ile Cys Lys Ala Leu Trp Cys His Arg		
265	610	615	620
267	Ile Gly Arg Lys Cys Glu Thr Lys Phe Met Pro Ala Ala Glu Gly Thr		
268	625	630	635
270	Ile Cys Gly His Asp Met Trp Cys Arg Gly Gly Gln Cys Val Lys Tyr		
271	645	650	655
273	Gly Asp Glu Gly Pro Lys Pro Thr His Gly His Trp Ser Asp Trp Ser		
274	660	665	670
276	Ser Trp Ser Pro Cys Ser Arg Thr Cys Gly Gly Val Ser His Arg		
277	675	680	685
279	Ser Arg Leu Cys Thr Asn Pro Asn Pro Ser His Gly Gly Lys Phe Cys		
280	690	695	700
282	Glu Gly Ser Thr Arg Thr Leu Lys Leu Cys Asn Ser Gln Lys Cys Pro		
283	705	710	715
285	Arg Asp Ser Val Asp Phe Arg Ala Ala Gln Cys Ala Glu His Asn Ser		
286	725	730	735
288	Arg Arg Phe Arg Gly Arg His Tyr Lys Trp Lys Pro Gln Asp Leu Cys		
289	740	745	750
291	Lys Leu Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Ser Leu Ser		
292	755	760	765
294	Asn Lys Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val		
295	770	775	780
297	Cys Ile Asp Gly Ile Cys Glu Xaa Gly Cys Asp Asn Val Leu Gly Ser		
298	785	790	795
300	Asp Ala Val Glu Asp Val Cys Gly Val Cys Asn Gly Asn Asn Ser Ala		
301	805	810	815
303	Cys Thr Ile His Arg Gly Leu Tyr Thr Lys His His His Thr Asn His		
304	820	825	830
306	Tyr His Met Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr		
307	835	840	845
309	Glu Met Asn Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg		
310	850	855	860
312	Arg Tyr Tyr Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr		
313	865	870	875
315	Lys Phe Ser Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro		
316	885	890	895
318	Glu Asn Leu Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu		
319	900	905	910
321	Leu Leu Phe Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met		
322	915	920	925
324	Pro Arg Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr		
325	930	935	940
327	Trp Ala Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Arg		
328	945	950	955
330	Cys Leu Pro Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Ser Ala Thr		
331	965	970	975

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 857, 858, 2383, 2963

Seq#:2; Xaa Pos. 283, 792

Seq#:23; N Pos. 2196, 2230, 2261, 2270, 2295, 2301

Seq#:34; Xaa Pos. 450

Seq#:65; Xaa Pos. 41

VERIFICATION SUMMARY

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L:96 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:840
M:341 Repeated in SeqNo=1
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:272
M:341 Repeated in SeqNo=2
L:1956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:2160
M:341 Repeated in SeqNo=23
L:3356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:448
L:6506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:32